

Amendments to the Specification

I. Please replace the paragraph on page 29, lines 15-22 with the following amended paragraph:

The term "nucleotide sequence complementary to the nucleotide sequence of Table 1" refers to the nucleotide sequence of the complementary strand of a ~~nucleic acid strand~~ nucleotide sequence having a SEQ ID NO: designated in ~~the GenBank accession referred to in~~ Table 1. The term "complementary strand" is used herein interchangeably with the term "complement". The complement of a nucleic acid strand can be the complement of a coding strand or the complement of a non-coding strand.

II. Please replace the paragraph on page 31, lines 10-24 with the following amended paragraph:

As used herein, the term "specifically hybridizes" or "specifically detects" refers to the ability of a nucleic acid molecule of the invention to hybridize to at least a portion of, for example, approximately 6, 12, 15, 20, 30, 50, 100, 150, 200, 300, 350, 400, 500, 750, or 1000 contiguous nucleotides of a nucleic acid designated in any one of ~~SEQ ID Nos: 1-146~~ SEQ ID NOS:1-180, or a sequence complementary thereto, or naturally occurring mutants thereof, such that it has less than 15%, preferably less than 10%, and more preferably less than 5% background hybridization to a cellular nucleic acid (e.g., mRNA or genomic DNA) encoding a different protein. In preferred embodiments, the oligonucleotide probe detects only a specific nucleic acid, e.g., it does not substantially hybridize to similar or related nucleic acids, or complements thereof.

III. Please replace the paragraph on page 85, lines 4-29 with the following amended paragraph:

In yet another embodiment, the invention provides methods for determining whether a subject is at risk for developing a disease, such as a predisposition to develop IBD, for example UC or CD, associated with an aberrant activity of any one of the polypeptides encoded by

nucleic acids of ~~SEQ ID Nos: 1-146~~ SEQ ID NOS:1-180, wherein the aberrant activity of the polypeptide is characterized by detecting the presence or absence of a genetic lesion characterized by at least one of (i) an alteration affecting the integrity of a gene encoding a marker polypeptides, or (ii) the mis-expression of the encoding nucleic acid. To illustrate, such genetic lesions can be detected by ascertaining the existence of at least one of (i) a deletion of one or more nucleotides from the nucleic acid sequence, (ii) an addition of one or more nucleotides to the nucleic acid sequence, (iii) a substitution of one or more nucleotides of the nucleic acid sequence, (iv) a gross chromosomal rearrangement of the nucleic acid sequence, (v) a gross alteration in the level of a messenger RNA transcript of the nucleic acid sequence, (vi) aberrant modification of the nucleic acid sequence, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild type splicing pattern of a messenger RNA transcript of the gene, (viii) a non-wild type level of the marker polypeptide, (ix) allelic loss of the gene, and/or (x) inappropriate post-translational modification of the marker polypeptide.

IV. Please replace the paragraph on page 89, lines 8-14 with the following amended paragraph:

Another aspect of the invention is directed to the identification of agents capable of modulating the growth state of an IBD cell. In this regard, the invention provides assays for determining compounds that modulate the expression of the marker nucleic acids (~~SEQ ID Nos: 1-146~~ SEQ ID NOS:1-180) and/or alter (for example, inhibit) the bioactivity of the encoded polypeptide.

V. Please replace Table 1 on pages 93-100 with the following amended Table 1:

Table 1

	UC	CD	Acc No. SEQ ID NO:	Gene Names	Chromosome	Microsatellite Markers
I	↑21.4	↑12.8	Y000787 1	MDNCF/IL-8	4q13-q21	D4S392-D4S2947
I	↑15.3		X54489 2	MGSA (GRO1)	4q21	D4S400-D4S1534
I	↑7.9		M57731 3	MIP-2 (GRO2)	4q21	D4S392-D4S2947
I	↑8.9	↑4.1	M28130 4	IL8	4q13-q21	D4S392-D4S2947
I	↑6.8	↑3.9	X57351 5	IP-10 IFITM2	11	pTEL-D11S1318
I	↑6		J04130 6	MIP-1β/SCYA4	17q21	D17S933-D17S800
I	↑3.4		X53800 7	MIP-2β (GRO3)	4q21	D4S400-D4S1534
I	↑3.2		M69203 8	MIP-1 MCP-1/SCYA2	17q21 17q11.2-q12	D17S933-D17S800 D17S1293-D17S933
I	↑4.6		X04500 9	pro-IL-1β	2q14	D2S293-D2S121
I	↑3.5		X53296 10	IL-1RA	2q14	D2S293-D2S121
I	↑3.3		X04602 11	IL-6	7q21	D7S829-D7S673
I	↑3		J03756 12	Growth hormone 2 (GH2)	17q22-q24	D17S794-D17S795
I	↓3.5		D16431 13	Hepatoma-derived growth factor (HDGF)	17q2-q24	D17S794-D17S795
I		↓4	M58286 14	TNF Receptor member 1A	12p13.2	D12S99-D12S358
II	↑35.5		S75256 15	Neutrophil lipocalin (HNL)	-	-
II	↑10.4		X99133 16	Neutrophil gelatinase-associated lipocalin (NGAL)	9q34	D9S1821-D9S159
II	↑8.7		X85781 17	Nitric oxide synthase (NOS2)	-	-
II	↑5.1		X65965 18	Mitochondrial superoxide dismutase (SOD2)	6q25.3	D6S442-D6S1581
II	↑5.5	↑4.6	M22430 19	Phospholipase A2, group IIA (PLA2G2A)	1p35	-
II	↑5.3		X51441 20	Serum amyloid A (SAA)	11p	-
II	↑3.9		J03474 21	Serum amyloid A (SAA1)	11p15.1	D11S921-D11S1369
II	↑3.7		M21119 22	Lysozyme	-	-
II	↑3.4		D00408 23	Cytochrome P450 IIIA, polypeptide 7 (CPY3A7) (CYP3A7)	7	D7S479-D7S2545
II	↓4.2		D14662 24	Anti-oxidant protein 2	1	D1S2790-D1S2640
II	↓4.4		X64177 25	Metallothionein	-	-
II	↓8		J03910 26	Metallothionein-1G (MT1G)	16q13	D16S3057-D16S514

II	↑9		X85771 <u>27</u>	Nitric oxide synthase 2	10	D10S1786-D10S541
III	↑155	↑17.8	L08010 <u>28</u>	Regenerating islet-derived 1 β (REG1B)	2p12	D2S286-D2S169
III	↑75	↑36.4	J05412 <u>29</u>	Regenerating islet-derived 1 α (REG1A)	2p12	D2S139-D2S289
III	↑9.7	↑10.2	L15533 <u>30</u>	Pancreatitis Pancreatitis-associated protein (PAP)	2p12	D2S169-D2S139
III	↑58.8		HG3566-HT3769 <u>31</u>	Zinc Finger Proteins	-	-
III	↑55.1	↑12.5	M87789 <u>32</u>	Ig γ 3 (IGHG3)	14q32.33	D14S65-qTEL
III	↑17.5	↑4.7	M26311 <u>33</u>	S100A9/calgranulin B	1q12-q22	D1S514-D1S2635
III	↑10.8	↑3.6	U08021 <u>34</u>	Nicotinamide N-methyltransferase (NNMT)	11q23.1	D11S1347-D11S939
III	↑5		M72885 <u>35</u>	GOS2	-	-
III	↑3.9	↑4.2	X65614 <u>36</u>	S100 calcium-binding protein (S100P)	4p16	-
III	↑3.9		U01691 <u>37</u>	Annexin AV (ANXA5)	4q28-q32	D4S2945-D4S430
III	↑3.7		U22431 <u>38</u>	Hypoxia-inducible factor 1α (HIF1A)	14q21-q24	D14S1038-D14S290
III	↑3.2		HG3494-HT3688 <u>39</u>	NF-116 NF-IL6	-	-
III		↑3.3	X99585 <u>40</u>	Suppressor of mif two 3 (SMT3H2)	8	D8S257-D8S508
III		↑3.1	U66617 <u>41</u>	SWI/SNF related regulator of chromatin (SMARCD1)	12q13-q14	D12S333-D12S325
III		↑3.2	L19067 <u>42</u>	NF-kappa-B p65 subunit	-	-
III	↓3.1	↓3.2	D14520 <u>43</u>	Basic transcription element binding protein (2BTEB2)	-	-
III		↓3.2	M21142 <u>44</u>	Guanine nucleotide-binding protein α (GNAS1)	20q13.2-q13.3	D20S183-D20S173
III	↓6	↓4.9	AD000684 <u>45</u>	Liver specific bHLH-zip	-	-
III	↓3.1		S37730 <u>46</u>	Insulin-like growth factor binding protein 2 (IGFBP2)	2q33-q34	D2S137-D2S164
III	↓3.8		L11672 <u>47</u>	Zinc finger protein 91 (ZNF91)	19p13.1-p12	-
III	↓3.8		D32257 <u>48</u>	Transcription factor IIIa	13q12.3-q13.1	D13S221-D13S1244

III	↓5.5	↓3.3	M32886 <u>49</u>	Sorcin (SRI)	7q21.1	D7S524-D7S657
III	↓12.5	↓5.9	M16364 <u>50</u>	Creatine kinase, brain (CKB)	14q32	D14S65-qTEL
III	↑3		X52560 <u>51</u>	CCCAAT/enhancer binding protein	20q13.1	D20S109-D20S196
III		↓3	NM_001913 <u>52</u>	Cut (Drosophila) like-1	7q22	D7S479-D7S2545
III		↓12	L37127 <u>53</u>	POLR2J	7q22-q31.1	D7S479-D7S2420
III	↓7	↓6	L39060 <u>54</u>	TATA-BP associated factor	1	D1S474-D1S439
IV	↑4.8		U21049 <u>55</u>	Epithelial Epithelial protein upregulated in carcinoma (DD96)	-	-
IV	↑3.5		D38583 <u>56</u>	Calgizzarin (S100A11)	7, 17, 4	D7S529-D7S4 84, D717s1352-D17S785 D4S1615-D4S1579
IV		↑3.2	L42176 <u>57</u>	Downregulated in rhabdomyosarcoma (DRAL)	2q12-q14	D2S113-D2S176
IV	↓3.5		L07648 <u>58</u>	Max-interacting protein 1 (MXI1)	10q24-q25	D10S597-D10S1681
IV	↓4.4		L02785 <u>59</u>	Down regulated in adenoma (DRA)	7q31	D7S2420-D7S523
IV	↓5		U29091 <u>60</u>	Selenium binding protein	1q21-q22	D1S514-D1S2844
V	↑9.2		M57466 <u>61</u>	HLA-DPB1	6p21.3	D6S1558-D6S1616
V	↑5.9		HG3576-HT3779 <u>62</u>	MHC II β W52	-	-
V	↑5		HG1872-HT1907 <u>63</u>	MHC Dg	-	-
V	↑4.9		M33600 <u>64</u>	HLA-DRB1	6p21.3	D6S1558-D6S1616
V	↑4.1		X00274 <u>65</u>	HLA-DR α heavy chain	-	-
V	↑4		X62744 <u>66</u>	HLA-DMA	6p21.3	D6S1558-D6S1616
V	↑4		M16276 <u>67</u>	MHC II HLA-DR2-Dw12 DQw1-β	-	-
V	↑3.4		X03068 <u>68</u>	HLA-D II antigen DQw1.1 β	-	-
V	↑10.8		X57809 <u>69</u>	Ig λ gene cluster (HGL @)	22q11.1-q11.2	D22S420-D22S1144
V	↑9	↑3	L23566 <u>70</u>	Ig heavy chain, VDJRC	-	-
V	↑8.6		L02326 <u>71</u>	Ig λ-like polypeptide 2 (IGLL2)	22q11.2	D22S1144-D22S280

V	↑6.8		M63438 <u>72</u>	Ig rearranged γ chain, V-J-C region	-	-
V	↑5.6		X72475 <u>73</u>	Rearranged Ig κ light chain	-	-
V	↑4.6		M13560 <u>74</u>	Ia-associated invariant γ -chain (CD74)	-	-
V	↑4.1		M34516 <u>75</u>	Ω light chain protein 14.1	-	-
V	↑4		X73079 <u>76</u>	Polymeric Ig receptor	-	-
V	↑3.7		S71043 <u>77</u>	Ig alpha 2 - IgA heavy chain allotype 2	-	-
V	↑3.7		X00437 <u>78</u>	T-cell specific protein/T-cell receptor	-	-
V	↑5.9		J03909 <u>79</u>	Interferon γ -inducible protein 30 (IFI30) (IP30)	19p13.1	D19S899-D19S407
V	↑3		M63838 <u>80</u>	Interferon γ -inducible protein (IFI16)	-	-
V		↑4.8	D28915 <u>81</u>	Microtubular aggregate protein p44	1	D1S203-D1S2865
V	↓4.2	↓3.4	M13755 <u>82</u>	Interferon stimulated protein 15-kDa (ISG15)	1	D1S243-D1S468
V		↓3.4	D11086 <u>83</u>	IL-2 receptor γ chain (IL2RG)	Xq13.1	DXS983-DXS995
V	↓3	↓6	M84526 <u>84</u>	Complement factor D (DF)	-	pTEL-D19S413
V	↓3.9		M38690 <u>85</u>	CD9 antigen	12p13	D12S99-D12S358
V	↑5		M28590 <u>86</u>	MHC Dg	6	-
VI	↑20.4	↑40.8	M97925 <u>87</u>	Defensin 5 (DEFA5)	8pter-p21	D8S552-D8S549
VI	↑6.8	↑7.7	U33317 <u>88</u>	Defensin 6 (DEFA6)	8pter-p21	D8S277-D8S550
VII	↑16.2	↑3.3	L23808 <u>89</u>	MMP-12 (Macrophage elastase)	11q22.2-q22.3	D11S1339-D11S1343
VII	↑6.4		J05070 <u>90</u>	MMP-9 (Gelatinase B)	20q11.2-q13.1	D20S119-D20S197
VII	↑4.7		X54925 <u>91</u>	MMP-1 (Interstitial collagenase)	11q22.3	D11S1339-D11S1343
VII	↑4.2		X05232 <u>92</u>	MMP-3 (Stromelysin 1)	11q22.3	D11S1339-D11S1343
VII	↑13.3	↑3.8	L10343 <u>93</u>	Elastase specific inhibitor (Elafin)	20q12-q13	D20S119-D20S197
VII	↑11	↑3.1	Z74616 <u>94</u>	COL1A2	2q37	D2S2158-D2S125

VII	↑7.3		X52022 <u>95</u>	COL6A3	2q37	D2S2158-D2S125
VII	↑6.9	↑3.6	M55998 <u>96</u>	COL1A1	17q21.3-q22	D17S791-D17S794
VII	↑4.8		X06700 <u>97</u>	COL3A1	2q31	D2S2257-D2S115
VII	↑4.7		X15882 <u>98</u>	COL6A2	21q22.3	-
VII	↑3.9		X05610 <u>99</u>	COL4A2	13q34	D13S285-qTEL
VII	↑3.7	↑3.3	HG2157- HT2227 <u>100</u>	Mucin 4 (MUC4)	3q29	-
VII	↑3.1		X52003 <u>101</u>	Trefoil factor 1 (TFF1)	21q22.3	D21S1259-qTEL
VII		↑4.6	M22406 <u>102</u>	Intestinal mucin	-	-
VII	↑6.4		J03040 <u>103</u>	Osteonectin (SPARC)	5q31.3-q32	D5S436-D5S470
VII	↑4	↑3.2	X17042 <u>104</u>	Proteoglycan 1 (PRG1)	10q22.1	D10S210-D10S537
VII	↑3.9		D11428 <u>105</u>	Peripheral myelin protein 22 (PMP22)	17p12-p11.2	D17S804-D17S799
VII	↑3.8		X02761 <u>106</u>	Fibronectin 1 (FN1)	2q34	D2S137-D2S164
VII	↑3.7		M77349 <u>107</u>	Transforming growth factor beta-induced (TGFβI)	5q31	D5S393-D5S500
VII	↑3.2		D13666 <u>108</u>	Osteoblast specific factor 2 (OSF-2)	13	D13S267-D13S1253
VII	↑3.1		M10321 <u>109</u>	von Willebrand factor	12p13.3	D12S99-D12S358
VII	↑3		L09190 <u>110</u>	Trichohyalin (THH)	1q21-q23	D1S439-D1S459
VII		↑3.1	D88422 <u>111</u>	Cystatin A (CSTA)	3q21	-
VII		↑4.7	X58199 <u>112</u>	Adducin 2 (ADD2)	2p13-p14	-
VII		↑3.7	M86933 <u>113</u>	Amelogenin (AMELY)	Yp11.2	-
VII		↓3.2	D45370 <u>114</u>	Adipose specific collagen- like 2 (APM2)	10	D10S1786-D10S541
VII		↓3.8	X73501 <u>115</u>	Cytokeratin 20	-	-
VII	↓4		U60061 <u>116</u>	Zygin 2	2	D2S367-D2S2230; D2S177- D2S119
VII		↓3	AF006087 <u>117</u>	Actin-related complex	3	D3S3591-D3S1283
VII		↓6	D87460 <u>118</u>	Paralemmin	19p13.3	pTEL-D19S413
VIII	↑50.5		D28416 <u>119</u>	Esterase D (ESD)	13q14.1- q14.2	D13S328-D13S168

VIII	↑4.7		M15656 <u>120</u>	Aldolase B	9q21.3-q22.2	D15S202-D15S157
VIII		↑6.3	J04040 <u>121</u>	Glucagon (GCG)	2q36-q37	D2S156-D2S376
VIII		↓4.4	L31801 <u>122</u>	Monocarboxylate transporter 1 (MCT1)	1p13.2-p12	D1S418-D1S514
VIII	↓3		D10523 <u>123</u>	Oxoglutarate dehydrogenase (OGDH)	7p14-p13	D7S521-D7S478
VIII	↓4		M12963 <u>124</u>	Alcohol dehydrogenase 1a (ADH1)	4q21-q23	-
VIII	↓4.5		Y00339 <u>125</u>	Carbonic anhydrase II (CA2)	8q22	D8S275-D8S273
VIII	↓4.9	↓3.1	L10955 <u>126</u>	Carbonic anhydrase IV (CA4)	17q23	-
VIII	↓12.7	↓3.1	L05144 <u>127</u>	Phosphoenolpyruvate Phosphoenolpyruvate carboxykinase 1, soluble (PCK1)	20q13.31	D20S183-D20S173
VIII	↑3		U07158 <u>128</u>	Syntaxin 4A (STX4A)	-	-
VIII		↑3	L27706 <u>129</u>	Chaperonin subunit 6A (CCT6A)	7	D7S530-D7S509
VIII	↓7	↓3.1	J04093 <u>130</u>	UDP-glycosyl-transferase 1 (UGT1)	2	D2S2158-D2S125
VIII	↓3.2		U20499 <u>131</u>	Sulfotransferase family 1A (SULT1A3)	16p11.2	-
VIII	↓3		M15182 <u>132</u>	β-glucuronidase (GUSB)	7q21.11	-
VIII	↓4		U08854 <u>133</u>	UDP glucuronosyltransferase precursor (UGT2B15)	4q13	D4S1619-D4S392
VIII	↓5		D87292 <u>134</u>	Thiosulfate sulfurtransferase (TST)	22	D22S277-D22S283
VIII	↓13	↓4	M22324 <u>135</u>	Aminopeptidase N/CD13 (ANPEP)	15q25-q26	D15S202-D15S157
VIII	↓12	↑7	M22960 <u>136</u>	Protective protein for β beta-galactosidase (PPGB)	20q13.1	D20S119-D20S197
VIII	↑3.4		X90908 <u>137</u>	Fatty acid binding protein 6 (FABP6)	5q23-q35	-

VIII		↑4.1	J02874 <u>138</u>	Fatty acid binding protein 4 (FABP4)	8q21	-
VIII	↓3		M10050 <u>139</u>	Fatty acid binding protein 1 (FABP1)	11p15.5	D11S1318-D11S909
VIII	↓3		L24774 <u>140</u>	Mitochondrial d3, d2-CoA-isomerase	-	=
VIII	↓4		D16294 <u>141</u>	Mitochondrial 3-oxoacyl-CoA thiolase (ACAA2)	18	D18S1118-D18S474
VIII	↓4		M77144 <u>142</u>	3 h beta-hydroxysteroid dehydrogenase (HSD3B2)[(D)]	1p13.1	D1S418-D1S514
VIII	↓5		D10511 <u>143</u>	Mitochondrial acetoacetyl-CoA thiolase	-	-
VIII	↓7		Z80345 <u>144</u>	Acyl-Coenzyme A dehydrogenase (ACADS)	12q22-qter	D12S366-D12S340
VIII	↓7		L11708 <u>145</u>	17 h beta-hydroxysteroid dehydrogenase II (HSD17B2)	16q24.1-q24.2	D16S515-D16S422
VIII	↓7		U26726 <u>146</u>	11 h beta-hydroxysteroid dehydrogenase II (HSD11B2)	16q22	D16S3031-D16S3139
VIII	↓3.5		X93036 <u>147</u>	MAT8 protein	19	D19S425-D19S418
VIII	↓12.2	↓4	M97496 <u>148</u>	Guanylate cyclase activator 1B 2A (UCA1B) (GUCA2A)	6p21.1	D1S2843-D1S417
VIII		↑4.2	D17400 <u>149</u>	6-pyruvoyl-tetrahydropterin synthase (PCBD) (PTPS)	10q22	D10S210-D10S537
VIII		↑3.3	D21262 <u>150</u>	KIAA0035	-	-
VIII		↑3.1	AB002365 <u>151</u>	KIAA0367	-	-
VIII		↓4.5	M11119 <u>152</u>	Endogenous retrovirus envelope region	-	-
VIII	↓3.1		M19964 <u>153</u>	Mitochondrial cytochrome c oxidase Vb (COX5B)	2cen-q13	D2S113-D2S176
VIII	↓3.1		D26129 <u>154</u>	Pancreatic ribonuclease (RNASE1)	14	pTEL-D14S283
VIII	↓3.1		U77643 <u>155</u>	K12 (SECTM1)	17q25	-
VIII	↓4		HG3991-HT4264 <u>156</u>	Cpg CpG-Enriched DNA, clone E18	=	=
VIII	↓3		U84388 <u>157</u>	CRADD	2q21-q33-q23	D12S327-D12S1657
VIII	↓3		M82962 <u>158</u>	Meprin 1A	6p12-p11	D6S1616-D6S427
VIII	↓4		X17059 <u>159</u>	N-acetyl-transferase 1	8p23.1-p21.3	D8S549-D8S258
VIII	↓4		M60483 <u>160</u>	Protein phosphatase 2CA	5q23-q31	D5S471-D5S393
VIII	↓4		M69023 <u>161</u>	Tetraspanin-3	17q21	D17S933-D17S800
VIII		↓3	D63391 <u>162</u>	PAF acetylhydrolase	19q13.1	D19S425-D19S418
VIII		↓3	X64559 <u>163</u>	Tetranectin A	3p22-p21.3	D3S1260-D3S1588
VIII	↓4		M25629 <u>164</u>	Kallikrein 1	19q13.3	=
VIII	↓4		U16660 <u>165</u>	Enoyl CoA hydratase 1	19q13.1	=

VIII	↓19		X83618 <u>166</u>	Mitochondrial HMG Co A Synthase 2	1p13-p12	D1S4718-D1S514
VIII	↓4	↓4	D83782 <u>167</u>	SREBP cleavage activating protein	=	D3S3582-D3S1588
VIII	↓4	↓5	Z70295 <u>168</u>	Guanylate cyclase activator 2B	1p34-p33	D1S2843-D1S417
VIII	↓12		J04444 <u>169</u>	Cytochrome C1	8q24.3	D8S272-qTEL; D7S2493-D7S529
VIII	↓54		L77701 <u>170</u>	COX17	13	D13S1253-D13S168
VIII		↓3	L38487 <u>171</u>	Estrogen receptor α	11q12	D11S3913-D11S916
VIII	↓3		M16801 <u>172</u>	Mineral corticoid receptor 3C2	4q31.1	D4S1586-D4S1548
VIII		↓4	S49852 <u>173</u>	ATPase 2B1	12q21-q23	D12S102-D128327
VIII	↓4		D16469 <u>174</u>	ATPase 6S1	Xq28	DXS1193-qTEL, D2S110-D2S312
VIII	↓3		L20859 <u>175</u>	SLC20A1	2q11-q14	D2S293-D2S121
VIII	↓4		U14528 <u>176</u>	SLC26A2	5q31-q34	D5S436-D5S470
VIII	↓6	↓3	M14758 <u>177</u>	ATP binding cassette B1	7q21.1	D7S524-D7S657
VIII	↓5		U90543 <u>178</u>	Butyrophilin 2A1	6p21.3	D6S1660-D6S1558
VIII	↓7		M29610 <u>179</u>	glycophorin E	4q28-q31	D4S1579-D4S1604; D4S1604-D4S1586
VIII	↓3		D14811 <u>180</u>	KIAA0110	6	D6S1558-D6S427

VI. Please insert the accompanying paper copy of the Sequence Listing, page numbers 1-157, at the end of the application.